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ST8- Biological Network Analysis in Computational Biology and Biomedicine

Call for Papers

The developing of high-throughout innovative technologies (e.g. next generation sequencing, microarray, and mass spectrometry) made it possible to reveal the comprehensive network of interactions that govern complex diseases. As a result, the need for new more efficient analysis and representation methodologies than conventional arise. These new methodologies should be able to help the researcher to spur light in the behavior of complex biological network diseases such as cancer, diabetes, and alzheimer. Graph theory offers a solution to represent and extract relevant insight from large biological interaction networks. As a result, to understand better the behavior of complex interactions network, the study of network dynamics as well as network topology, have been a primary point in Bioinformatics research.

Nevertheless, these studies are challenging because of the large scale and complex connectivity of current biological networks data sets, provided through high-throughput experimental data set.

Several computational techniques ranking from graph-mining to statistics might be applied for the efficient analysis of the large-scale interaction biological networks. Lately, the application of such techniques applied to personalized and translational medicine is becoming the central area. In fact, as methodologies evolve, network analysis has the potential to discover the complexity of molecular mechanisms governing complex diseases as well as, to drive researchers to develop new drugs by revolutionizing the process of drug discovery.

Many research problems in current high-throughput interactome data are still open, such as the integration of existing databases is an essential task to obtain a detailed map of interactions. Moreover, the use of semantic technologies to query, analyze and organize data, the definition of novel paradigms to represent the dynamics of fluxes through the interactome, and finally, the integration of multiple data set coming from heterogeneous sources (i.e. protein, DNA, RNA, and microRNA), are emerging research topics.

This special track aims to bring together researchers in bioinformatics and biomedicine with the objective to discuss the current state of biological networks analysis, focusing mainly on applications to biomedicine, and sharing the best practice guidelines for reporting the fundamental principles of biological network theory in medicine, and an opportunity to facilitate interdisciplinary collaborations.

Topics

Topics of interest include, but not limited to:

- Biological network representation
- Function prediction from biological networks
- Motif analysis in biological networks
- Functional pathway identification, integration and visualization
- Protein complex or functional module detection

- Molecular interaction prediction
- Network dynamics and evolution analysis
- Network data management and integration
- Graph mining algorithms
- Querying and retrieval of PPI data
- Semantic web technologies for Interactomics
- Parallel or grid-based approaches for Interactomics
- Biomarker discovery (identification of molecular targets for early detection, prognosis and treatment of diseases)
- Integration and analysis of genomic, proteomic, and interactomic data for medical applications
- Technologies and data models for phenotype, genotype and prototype data

Paper submission guidelines

Please follow the general conference paper submission guidelines that can be found here: http://www.cbms2017.org/content/call-for-papers

Important dates

Paper submission due (general and special tracks)	January 30, 2017
Notification of acceptance for papers	March 20, 2017
Final camera-ready paper due	April 13, 2017
Early registration deadline	April 23, 2017
IEEE CBMS 2917 conference days	June 22-24, 2017

Special Track Chairs

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